

\Sa247851\_0026.Dna  
Gcg\_Geneseq\_D:T19113

XP2128499

ID T19113 standard; cDNA to mRNA; 351 BP.  
AC T19113;  
DT 04-JUL-1996 (first entry)

DE Human gene signature HUMGS00127.  
KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
KW human; cloning; mapping; non-biased library; diagnosis; detection;  
KW cell typing; abnormal cell function; ss.  
OS Homo sapiens.  
PN WO 9514772-A1.  
PD 01-JUN-1995.  
PF 11-NOV-1994; 94WO-JP01916.  
PR 12-NOV-1993; 93JP-0355504.  
PA (MATS/) MATSUBARA K.  
PA (OKUB/) OKUBO K.  
PI Matsubara K, Okubo K;  
DR WPI; 1995-206931/27.  
PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
PT for diagnosis of abnormal cell function, by preparing cDNA that  
PT reflects relative abundance of corresp. mRNA in specific human  
  
PT tissues  
PS Claim 1; Page 304; 2245pp; Japanese.  
CC A single-stranded DNA (or its complementary strand or the corresp.  
CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
CC given in T19001-T26837 and which is able to hybridise to part of  
CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)  
CC sequences were obtained from 3'-directed cDNA libraries prepared  
CC from various human tissues; synthesis of cDNA was initiated from the  
CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
CC untranslated sequence is unique to a particular mRNA species, almost  
  
CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library  
CC is constructed so as to reflect accurately the relative abundance of  
CC different mRNAs in the particular tissue from which it was derived.  
CC The appearance frequency of a given GS in a cDNA library can be  
CC determined (esp. using primers and probes derived from the GS  
CC sequences) as a means of diagnosing abnormal cell function or for  
CC recognising different cell types.  
SQ Sequence 351 BP; 123 A; 45 C; 58 G; 121 T; 4 other;

SCORES Init1: 1638 Initn: 1638 Opt: 1706 z-score: 597.6 E(): 5.9e-24  
98.9% identity in 349 bp overlap

	1480	1490	1500	1510	1520	1530	
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T19113							
				GATCACATTATNATAAAATAATGAAAAAAT			
					10	20	30
	1540	1550	1560	1570	1580	1590	
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T19113	GATTTAACCTGTAATAAAACTGGTTATTGTGCAGTGACTGTAATATACTAGAGTTATAAT						

40 50 60 70 80 90

1600 1610 1620 1630 1640 1650  
Sa247851\_002 AAATTGTTACTCTGCCTCACCAAACACATGCTAGGATATAACCCCCAAAATAAGTATT  
T19113 AAATTGTTACTCTGCCTCACCAAACACATGCTAGGATATAACCCCCAAAATAAGTATT  
100 110 120 130 140 150

1660 1670 1680 1690 1700 1710  
Sa247851\_002 AACTTGCATTAGGTATAAAGGAGACTGGGTGCTATAATTAGATTATTTGAGGCAGACA  
T19113 AACCTTGCAATTAGGTATAAAGGAGACTGGGTGCTATAATNAGATTATTTGAGGCAGACA  
160 170 180 190 200 210

1720 1730 1740 1750 1760 1770  
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T19113 ATACTTTTAGTGATTACATGTACATTTATAGGGGACATGTTCTGTGTATAGCGAATA  
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1840 1850 1860 1870  
Sa247851\_002 AATAACTTTATAGTATCAAAAAAAAAAAAAAA  
T19113 AATAACTTTATAGTATCACN  
340 350



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(12)

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(71) Applicant: Matsubara, Kenichi  
Room 804, 18-1, Yamadaishi-gashi 3-chome  
Sulta-shi,  
Osaka 565 (JP)  
Applicant: Okubo, Kousaku  
11-26, Segawa 2-chome  
Minoo-shi,  
Osaka 562 (JP)

(72) Inventor: Matsubara, Kenichi  
Room 804, 18-1, Yamadaishi-gashi 3-chome  
Sulta-shi,  
Osaka 565 (JP)  
Inventor: Okubo, Kousaku  
11-26, Segawa 2-chome  
Minoo-shi,  
Osaka 562 (JP)

(74) Representative: Vossius, Tilman et al  
Dr. Volker Vossius,  
Patent- und Rechtsanwaltskanzlei,  
Holbeinstraße 5  
D-81679 München (DE)

(54) GENE SIGNATURE.

(57) A 3'-directed cDNA library which accurately reflects the abundance ratio of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has been conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce proteins utilizable as a medicine or the like.

Table 1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT:

- (A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
- (B) STREET: 41-8, Takada 3-chrome, Toshima-ku
- (C) CITY: Tokyo
- 10 (E) COUNTRY: JAPAN
- (F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

15 (iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
- (B) COMPUTER: IBM PC compatible
- 20 (C) OPERATING SYSTEM: PC-DOS/ MS-DOS
- (D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

- (A) APPLICATION NUMBER: EP 95900295.7

25 (vi) PRIOR APPLICATION DATA

- (A) APPLICATION NUMBER: PCT/JP94/01916
- (B) FILING DATE: 11. November 1994

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5           SEQ ID NO:7844  
SEQUENCE LENGTH:37  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTCGCTCGCC CATCCTTATA CAGGCTCACT TTTGTCT           37

10          SEQ ID NO:7845  
SEQUENCE LENGTH:37  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTCGCTCGCC CATGTATAGG GACAGCATT CTGAGAG           37

15          SEQ ID NO:7846  
SEQUENCE LENGTH:38  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG           38

20          SEQ ID NO:7847  
SEQUENCE LENGTH:22  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
CCAGGGTTTT CCCAGTCACG AC           22

25          SEQ ID NO:7848  
SEQUENCE LENGTH:22  
SEQUENCE TYPE:nucleic acid  
STRANDEDNESS:single  
TOPOLOGY:linear  
SEQUENCE DESCRIPTION:  
TCACACAGGA AACAGCTATG AC           22

50 Claims

- 55 1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA , a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.  
5
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.  
10
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.  
15
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.  
20
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.  
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Fig. 1

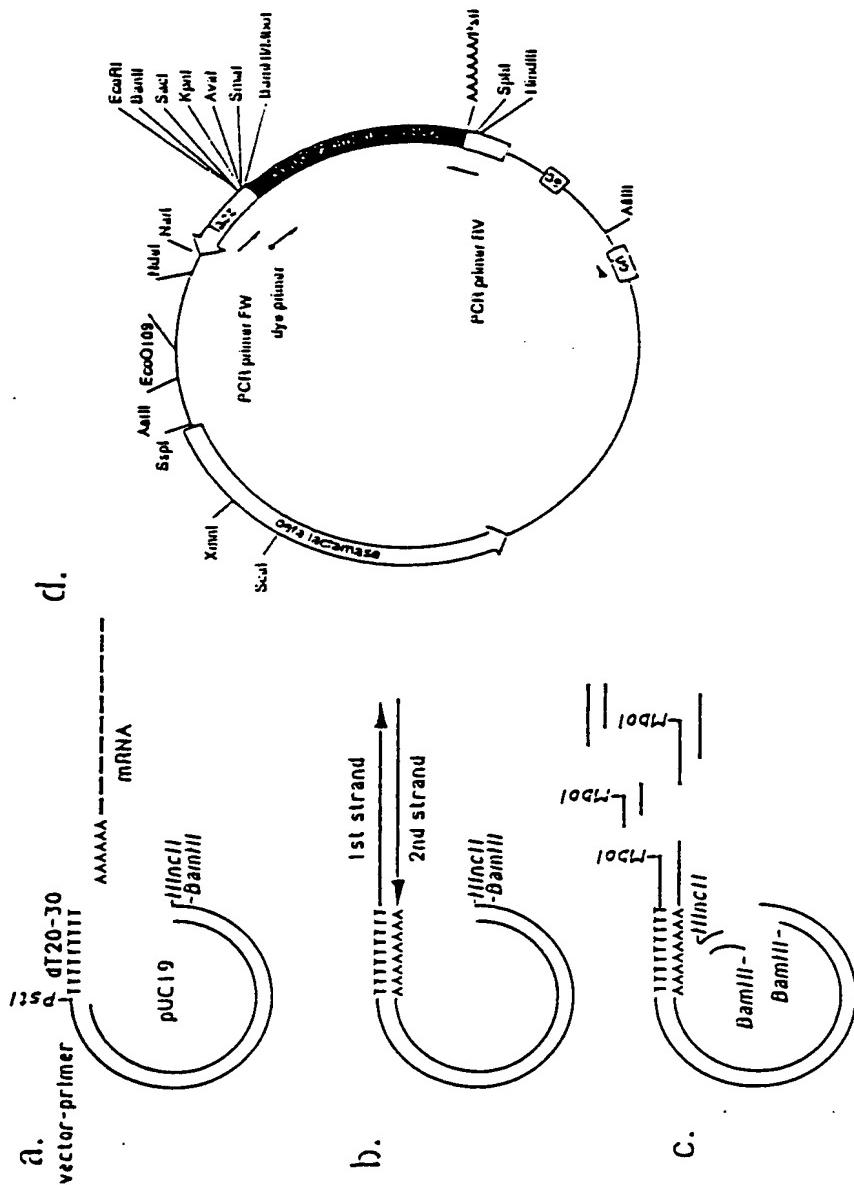


Fig. 2

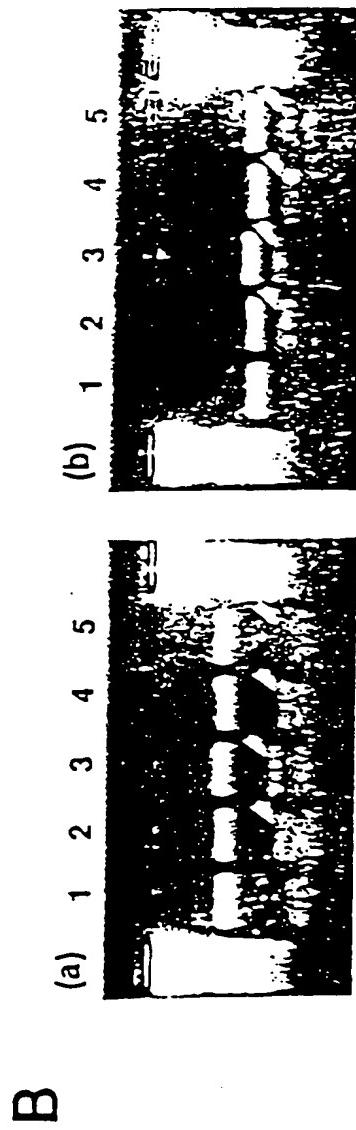
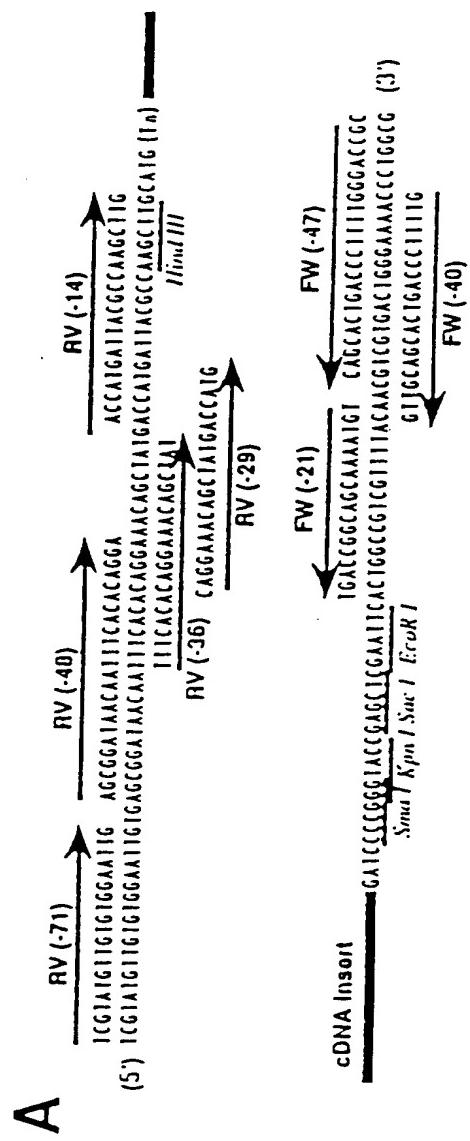


Fig. 3

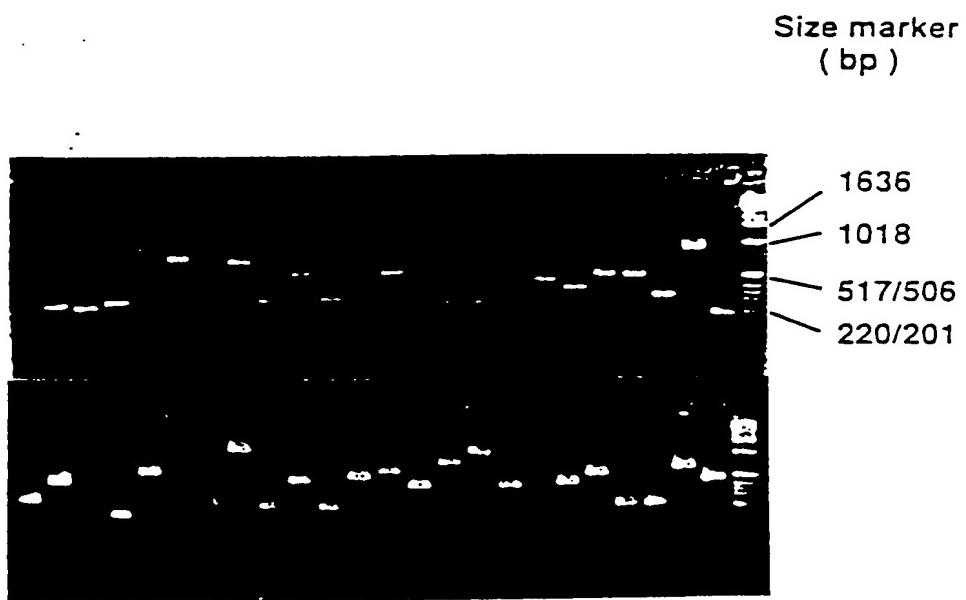


Fig. 4

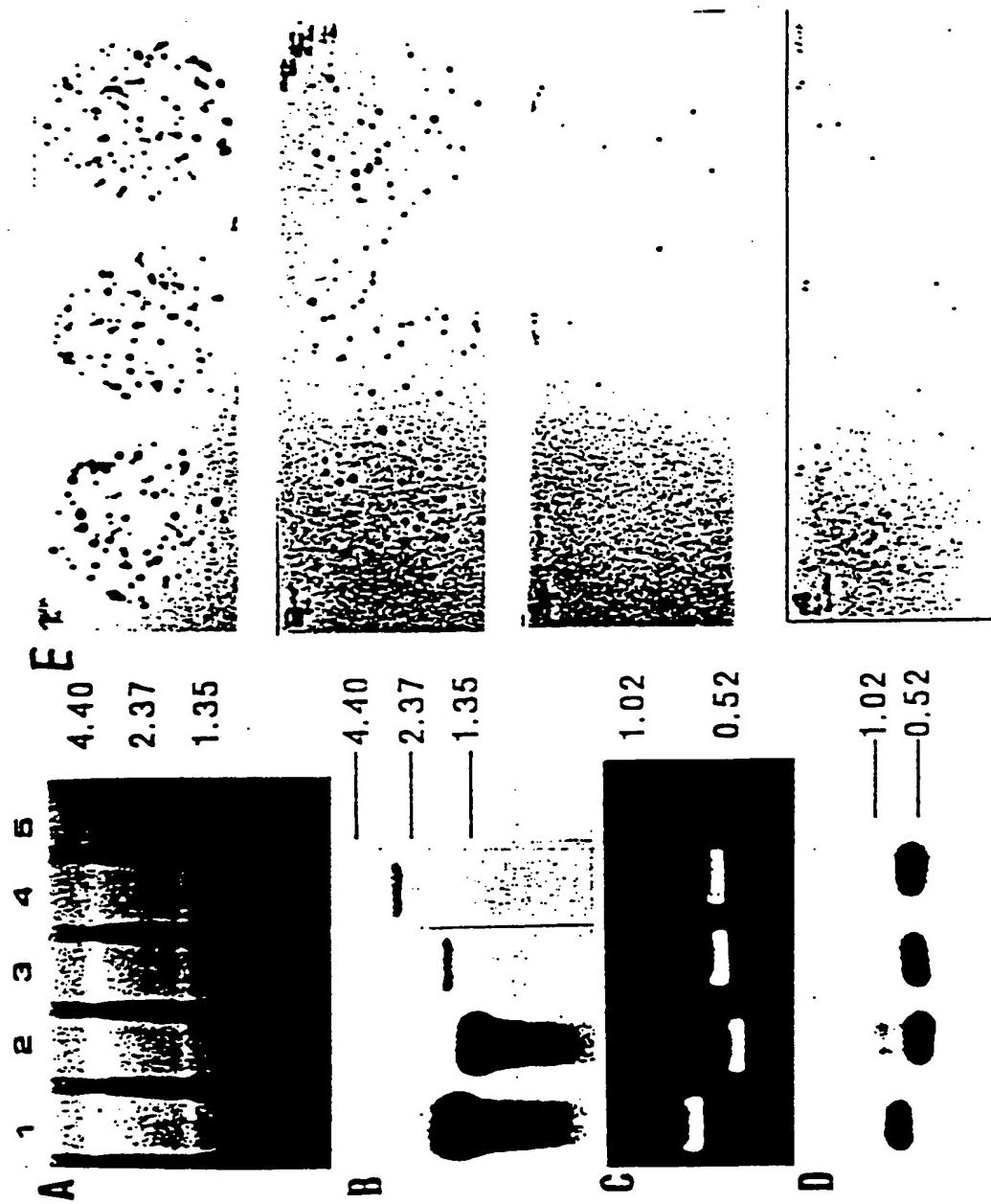


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- $\alpha$	$\alpha$ 1-antitrypsin	HnRNP core protein A1	Inter- $\alpha$ -tryptsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

## Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A in 902 (%)	B "in 8,800 (%)"	C "in 26,400 (%)"
	a15	Elongation factor - 1 $\alpha$	22 (2.2)	307 (3.5)	NT
I	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	lb030	$\alpha$ -1-antitrypsin	0 (0.0)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP (II) Menadione oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	lb042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
	s155	unknown	1	2	5 (0.02)
	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
	s635	unknown	1	0	2 (0.01)
II	s170	unknown	1	0	1 (0.001)
	s154	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s645	unknown	1	0	1 (0.004)
	s647	unknown	1	0	0 (<0.001)
	s632	unknown	0	0	0 (<0.001)

Fig. 6

GS	CI	Chromosomal position	Sequences of primers		AT	TTO	TIE	TIO	CO	G	T
			Sense	Anti-sense							
§1600184	pm12166	-	CAGGCCCGTAGAACAT	AAGTTATGTGGGTCAG	48	114	115	104	110	1	2
§1601024	pm12144	-	AATGGGACAGTTAGCTGA	CCAGCTCCCTGACTGAA	44	61	81	>200	1	-	-
§1601035	pm12081	-	TGGACTGGTACCTATCT	ACAGTACCCGAAAGCT	44	124	124	103	107	4	4
§1601047	pm12172	-	GICACTCTGCCATGAC	ACCACTCTGCCACACT	50	104	104	100	>200	6	6
§1601094	pm12147	-	GCCCCAACGAGGAAC	TAATTCACCTCCGTAC	51	114	116	>200	200	-	-
§1601116	pm12171	-	GGTTTCAATAGGTGACC	GCCCCAACGAAACG	49	95	95	76	107	-	-
§1601191	pm12049	-	TGGCGATTGACATTGTTG	GGCTGACATCAGCTTG	47	97	97	-	200	-	-
§1601200	pm12151	-	TTAAGAGACCTTATGGACC	ATAATCTGGTATGACATAC	47	97	98	-	200	-	-
§1601216	pm12082	-	TCAGGTCGCTGGAGATG	AACTACAGCACAGTAITG	51	120	122	>200	>200	-	-
§1601446	pm12110	-	AGGTGTAAGGATATTGAGA	TGCATAGCCAACTCAT	47	130	125	>200	>200	-	-
§1601464	pm12139	-	CCAAAGACCTCGGTAAACA	TTGGGAGGCTATGACAG	51	100	100	>200	-	-	-
§1601468	pm12127	-	TACTCTGGAAAGTAAAC	CAGGGACCATTTCTTA	40	98	98	-	-	2	2
§1601521	pm12185	-	CCCAAATCAATGTTAAATG	TTTGATCAGAGATGAGT	43	102,175	100	>200	>200	-	-
§1601534	pm12291	-	CCAGAGAGTCAGGGATG	GCTACAGATGCAAGACT	46	57	57	78	155	-	-
§1601572	pm12006	1	CCACATGTTCTGACTG	AAACTTATGGCTCCT	44	58	58	>200	>200	-	-
§1602120	pm11350	2	CATGATCTCTGGTGGTAA	AAACAGTAGTGGCAGAT	45	84	103	-	-	-	-
§1601636	pm11720	2	AGCTGAAATGGGGCATCT	CCGGTTATGCTACAGCT	48	119	119	91	115	-	-
§1601681	pm10931	2	AAAGCAATACAAATTACCAA	TICATAATGTTAACAGTA	40	90	90	-	-	-	-
§1602925	pm12050	2	TAIAGTACACGATGAAATG	TAIAGTAAATGCGGTAA	45	88	88	-	-	-	-
§1602110	pm12010	2	CCAGAATGAGGGAACTCT	CTGGAAATGAGAACAAACAG	47	125	125	130	>200	-	-
§1602915	pm12035	2	TCAGATTTGCTCTTAA	GGAAATATGCTCTAGTG	43	103	103	-	-	-	-
§1602903	pm12093	2	AGTCCTCTGGCTCTCAT	TAICGTCAGGCCCTTATG	52	117	117	>200	-	-	-
§1602335	pm12135	2	TTTGGCTCTGCTGAGACTT	ATCGTGGCACACATAGTA	45	105	108	-	-	2	2
§1601412	pm11671	2	TTTATGGCTGCTTATCTG	AGTCACATCTGGTATGAG	45	67	65	>200	>200	-	-
§1601453	pm12145	2	TIGCTCTGGCTCTAATG	ATGATATGACAAATCAAG	45	75	75	170	190	-	-
§1601535	pm1216	2	ATCTAGTTGTTGAGATG	AGCTATTTGCTCTCATG	44	68	67	-	-	-	-
§1600875	pm12149	3	CGAACATTCACCTCTATA	ATGATTATTTAGGAGAA	43	68	68	-	-	3	6
§1601101	pm11754	3	TCTGGCTCTGGTGGAA	GGCCACAGAGTACAGTC	51	115	115	-	-	-	-
§1601214	pm12134	3	AAAAGAACGACTCTAA	ATGATATGACAAATCAAG	42	90	90	-	-	-	-
§1606688	pm12119	3	GTAGTCCTCTGCCCTTGC	AGGATTGATTCAT	43	77	77	-	-	-	-
§1601229	pm12129	3	GGCTCTGTTATTTGACAT	AAACAGAGGAGGTCAGA	43	75	75	155	>200	-	-
§1601206	pm11022	3	GATCCCTGTTGTTGTC	CTGAAATACAGGGATCAT	46	83	83	160	140	-	-
§1601114	pm12049	3	ACCCAGTCACATCCAGT	ACACTCCCACCCCTACT	55	105	105	113	>200	-	-
§1601165	pm12155	3	ATCTAGTGGCTGTGATAT	TTAAGAGATGAATTATGGT	42	130	130	130	>200	-	-
§1600271	pm12122	4	GTCCTTGCTCTGCTGTA	AAAGATTTTGGGTTAA	43	90	90	95	>200	-	3

Fig. 7

91000448	pmn1151	GACCAAGTTCTCTTGTAT	42	62	>200	69	2
91001032	pmn0988	GTGCCATGACTGTGTTAT	43	80	-	-	1
91001215	pmn2167	AGAAAATTATAGCATAGGT	43	100	130	-	1
91001238	pmn0997	ATCAAAGTTATGCTCA	43	116	>200	160	1
91000994	pmn1689	TCTCTGAAGCAGCACAA	43	116	>200	160	1
91001065	pmn0119	AAGCAATGCCATCACAG	43	101	113	200	1
91001101	pmn2264	TCACCCATCACATCAAGTC	43	87	>200	>200	1
91001161	pmn1150	TCTCTGAAGCAGCACAA	43	104	145	200	1
91000952	pmn2220	AAGCAATGCCATCACAG	43	89	93	>200	1
91001226	pmn1154	TCACCCATCACATCAAGTC	43	101	90	>200	200
91001234	pmn1216	TTACCTTACCGTGCTTAC	44	78	72	>200	200
91001557	pmn1785	ATTITGTAATGGTTTACTA	44	102	104	145	200
91001552	pmn0285	ATGTCATAGTCCTCTCA	44	65	65	110	200
91001523	pmn0228	CATTGACAGCAGCACAG	44	90	90	>200	>200
91001562	pmn2619	TADGCACAAACAGGAGAG	45	86	83	>200	200
91000624	pmn0191	TATATGAAATATCCAAAGCTG	45	119	119	>200	200
91001145	pmn0281	TTGTAACGTTGCTCAGT	45	139	155	115	>200
91001169	pmn2119	GCACCTAAGCICCCAAAGT	45	89	83	130	-
91001579	pmn1102	TCTGCAATTGCAAGAACCC	45	86	83	130	-
91001207	pmn0956	GACCTGAGTTGTAATGAGT	44	77	75	170	-
91001176	pmn2322	-AGCCAAACCTGGGGTAATCT	44	74	72	73	-
91001248	pmn2108	ATACATTGCGAGAAGCTGA	44	81	81	105	20
91000760	pmn0995	TCAGGAGTCGCTCAGTAA	44	99	99	110	180
91001055	pmn0559	TTMAGAATCCCTCATG	44	95	95	85	-
91001157	pmn0347	AGATATGTCGAAAGTGA	43	55	55	-	-
91001218	pmn2245	TGTGAATGCTATCTCTCT	44	74	74	72	-
91000228	pmn2661	ATCAAACACAACTCAGA	45	138	138	>200	200
91001159	pmn0880	GAATAGCTGGAGATTTCAC	47	100	100	200	-
91001115	pmn0445	AAAGTCACCTGATGGACACTG	42	117	121	124	95
91001352	pmn2043	TGAGTAGGGTATTTCAG	46	100	100	84	95
91001469	pmn0559	MCCCTCTAGTAAAGCTATG	47	93	93	-	2
91001570	pmn2810	CIGTAAGGTTTGGAAATATG	37	47	47	125	53
91000279	pmn0266	AGTGTATGAAACCTCTG	42	75,92	75	145	>200
91001163	pmn2156	TCTCCATATCACACAGT	48	130	130	103	>200
91001193	pmn1193	CACAGCATAAAGATATA	49	88	83	>200	120
91001215	pmn2790	CATCATGTTACAGTCAGAG	46	100	100	-	-
91001224	pmn1355	AGATGICAGATATCCTCATG	44	83	82	93	87
91001208	pmn0368	CAAAGGCTAGGGTACAO	47	95,165	95	>200	>200
91000153	pmn2645	CTAAGATTAATGGCATTC	46	104	104	>200	>200

Fig. 8

Fig. 9

91000999		X	CTACCATGTTACCTGATT	TACCCACCACTATTAGCA
91001149	pml1759	X	GGAGGGGAGATAATAGTGT	AAAAAACTGGAGAGACIGA
91001161	pml2180	X	TCTATTAATGTCACAGTT	GGAGATGTTGAAATACAT
91001165	pml5048	X	TAATGCCAGTGAATGTCGTA	GTAAGGTTTATCTGCACTAGA
91001169	pml1394	X	ATCGCTGAAATACATCTG	GGGGAGAACACATCATGAC
91001176	pml2249	1,18	GATCCATGGAGGTAAAT	AATACAAAGCTAACCCCAA
91001181	pml0113	1,2,12,13,Y	TIGGATGACATCTCTAT	TITATGTAACAAAGCACT
91001191	pml2222	1,2,3,5,8,12,14,17,X	TATCAAGCTGAAAATGTCAC	TACIGAATCCACCAACCA
91002003	pml0314	1,2,6,X	1,3,4,5,9,16	AGTIGACAGCAGGGTGAAG
91002010	pml1461	2,20,21,22	TCCAAATGAGGAGGTTA	TITTAATGTTGCTCAAGI
91002154	pml1561	2,4,5,10,12,15,17,20,22,Y	GTCCTACGCCAGATTGACT	TTAAATGGTTGTTACCTGG
91002156	pml2295	20,X	GCCTGTATTTCACCTCTC	ATCTCCCTTGGCCAGATA
91002177	pml0443	2,5,14,C	TCTGAGGACATCCAGACAG	AGTGACAAACACACGGTAT
91002192	pml1653	2,8,12	TGCAATAMGGAAACACCA	CGTTGTTAGGTTGAAATG
91002213	pml1776	2,9,13,17,X	GTCATTGTGTCATTCTCC	ACATTITATTTTCAACGG
91002219	pml0085	20,X	CATGIACTCAGGGCACITC	GCAACTACAAATCCAAACT
91002269	pml0157	3,10,15	CAGGGACTGGAGGAGAAAG	GATTAACTCATAGGAGGC
91002271	pml2651	3,4,M	TGAGGAAATAGGTTAGAG	ATAGTATGGTTGACACGTA
91002278	pml2632	3,6	TGGATTGCTTACCTGTT	ACACCICAGGAGTTTAC
91002279	pml1123	3,8	GCACIACAGGCCAACACGA	CITCTTAAACACACAGCAG
91002280	pml2250	3,9,10,15	GGATTCTTATGGCTGTAT	GTTATGTTGACGCAATTAC
91002635	pml0626	4,6	GCATTAAACGAAACATA	CTTCACGAGGCTAACCC
91002212	pml1234	6,20	AGAIGCTAACATTAGGATA	TTTATGACATAGGAGGAGI
91002212	pml0606	7,18	CCAGACTACGGCTGATGGC	CCCTTACCCAGGACACCTT
91002257	pml1253	9,11	ACCAGTCACGCTCTTAAATA	CCCATATAAAGTGAAGGAGTGTIC
91002261	pml0115	9,11	AAGAAATTTTACTGTT	TIAATGACTGGGAAAT
91002261	pml224	10,15,22	ACTACCCCTGAGATAATAGT	TICATTATGTTGATGTTGTA
91002261	pml2120	11,11	ATACCACTTCGGCTTCAG	GAGGAGGTCTCCTGGCTCT
91002261	pml2203	11,M	GCACCAAGAAGAGCTTCAG	TGGGGATGAAATAACT
91002261	pml2643	12,19	GATCTCAGTCCTGGTTATT	TACATACMAGAGGCAACAGT
91002261	pml2273	12,M	ATCTCTGTTGCTGCTTC	GTCCTCTCTCTGAGGCTG
91002261	pml1487	12,16	AACCTGTTTACCGCATCTT	AGGTTATGTCACCAAGAA
91002261	pml22780	14,16	TGTGTTGTCACCATGAGAC	AGMACACACATCAAGATGC
91002261	pml1683	17,20,C	GAATGTCATCCAGAGTAG	CTAGTATACTGGCTCTG
91002261	pml746	17,22,Y	TITATECCAGCAAGAAC	TGTCTCTCTCTCTCTCTC
91002264	pml0964	17,C	ACTTAAGTAGCTTGTACG	TGCTCTCTGCTGCTGATATA
91002269	pml2217	17,C	CCCAGTTAAAGATTTATGT	ATGAGGATGGAGGAGGAGA
91002140	pml213	18,C	TGCAAGAGGATTTCCAGAG	CTAGGTCATCTTCATCAG
91002177	pml1116	19,20	ATCCCTGCTCTATCAGAC	GCTCGTTAACDCTCTCAC
91002009	pml3024	19,22	GCCTACATCTGTTGTTACT	ACCTCTGGAAACAACTAT
91001172	pml0887	19,22		

Fig. 10

91001057	pm12049	C	AGGACACAAACACCAAGCTAT	TTCCTGATTAGACATGAC	45	75	75	101	75	-
91001177	pm1153	M	ATCTCTTGTAGCCATCCTA	GTTAAGCTGCTGATGCCATT	42	64,100	64	64	64	>200
91001056	pm12236	N	GTAGAGCTGCATGACTACC	ACAGACAGGAAATTCATA	42	100,06	110	110	112	-
91001168	pm1d596	N	GTCCCCACAGTCGCGCTAAC	CCACACATTTAGATCCATC	46	74	74	74	74	>200
91001151	pm12354	N	TGTCCTTGGAATCTGCCT	TITAACTCATTTATACATGTT	44	110	110	110	106	-
91000229	pm12492	M,C	GCTTAGAAGAGGGGACTICA	CITAACCTGATAGCCAGTC	46	75	75	75	75	-
91000231	pm12766	M,C	CAAAACACCAAACCTICAG	ATGGTTATTTCATGATG	41	03	03	82	83	2
91000235	pm11704	M,C	TCCACCCAGAGAAAGCACAT	ANTCATAGGGAAAGTC	40	75,130	75	75	75	3
91000302	pm12116	M,C	TCGAGAAGGACAAATTCACC	GAACAGGGTTAGTCATTCG	48	50	50	50	50	-
91000511	pm1689	M,C	CATGGGCTACGGAAACAGG	AGGACTCCGGGGCTCTGAG	51	01	04	84	84	18
91000615	pm11442	M,C	AAAGGATCTGAGAGGAAACA	GGAGGACTCTGGTGGCTCTA	49	110,200	110	110	110	-
91000722	pm1452	I,A,C	GGAGCAQATACCTTACACC	TGGTCTATTCTGGTCCCTC	51	102	105	102	102	2
91000995	pm1d268	M,C	GAAGGCTCTGGAGGAAGT	CAGACCCCATTTTAAACC	47	79	79	79	79	4
91001016	pm12703	M,C	ACGATATTATAGCTGAGTA	TCAAACCTTTATATATGCT	40	93	93	91	92	-
91001051	pm1144	M,C	AGATAGTGTGGGCTCAGAA	CCATCCCGTCTATCCAGTT	52	135	140	135	135	-
91001127	pm12290	M,C	ACTGCTGATGGAAAGTTACA	CCACACGIGAGGACCGCT	47	55	55	55	55	-
91001167	pm1625	M,C	GADACCCCTGGATCCTTA	CTTCCCCTGGCTGCTCTGT	49	100	100	100	100	-
91001216	pm12109	M,C	TAGTCAGATTCAGTAGT	ACAGTATTTTGTAGTCT	42	110	110	110	110	2
91001251	pm11240	M,C	AACGTTTCTCCATCAACTG	ACTGTTAAACCTCTCACC	40	120	120	120	120	-
91001281	pm1131	M,C	ACTAAAAACCCACCCGAT	ACMACAGCAGTCATAAGAA	47	97	97	97	97	-
91001315	pm10952	M,C	AAAGGAGATTCGGCTCTCA	ATCTGGAGAGGGAGGAGGA	51	09	09	09	09	-
91001356	pm12216	M,C	ATCTGATGACCTTATCT	CGTCTCTTCTTATGTCAT	45	100	100	100	100	-
91001411	pm1d958	M,C	ATGGGTTTATACGGGTTTC	GAGACCAAGGACCTCTA	47	uu	77	80	80	-
91001420	pm12626	M,C	ACATTTAGGGATGGATGAGGT	GGACATTCCTACCCACAGC	51	75,55	75	75	75	2
91001462	pm1210	M,C	TGTTGACATGGCTTCTGAA	CAGGCCCTCTGACTGAGACA	46	65	65	65	65	-
91001552	pm1d109	M,C	GCCCCAGAGACATCTCT	TCTTGTAGGACTCTGGTG	51	uu	uu	98	98	-
91001664	pm12012	No product	CAACCACTTGGGTGAAGT	GUATTAATCTCTGCTCTA	45	97	97	-	-	-
91000050	pm10204	No product	CTTGGGATATTCTCTCAT	CCCTGGGGTACTCTCTAG	43	60	60	62	-	2
91002661	pm10008	No product	AGCCAGCCCTCTGTAIGG	CTGGATTGATTCCTGATAG	44	87	87	-	112	-
91001152	pm1622	No product	TGTTGATGAAATATCTGA	TTTGTGATGAGACACACT	43	uu	90	163	>200	-
91001345	pm12908	No product	CAGTAGTGTGCTTGAATG	TTTATGTAATGCTGTGT	41	63	63	-	150	-
91001371	pm12061	No product	TACACCCACTCTAAAGTC	TTTGAGCATGAGGAATCT	45	02	02	-	>200	-
91001556	pm1d849	No product	TACATTCTCAGACTCTCG	TTTCAAAAACCTTATCTT	40	86	86	>200	100	-
91001514	pm12841	No product	ATCAAGGCTCAGTCCTGAG	ATTTCGCCTCTGATGGTC	44	57	57	67	67	2
91001622	pm16066	No product	GAATCTAGGCTTAACTGGA	TTTGGAGTCACTTTCATTC	45	54	54	-	-	-
91001640	pm10832	No product	GAATCTGTTCCCTTCA	TTTAAACAGACACATAC	36	45	45	-	-	-

Fig. 11

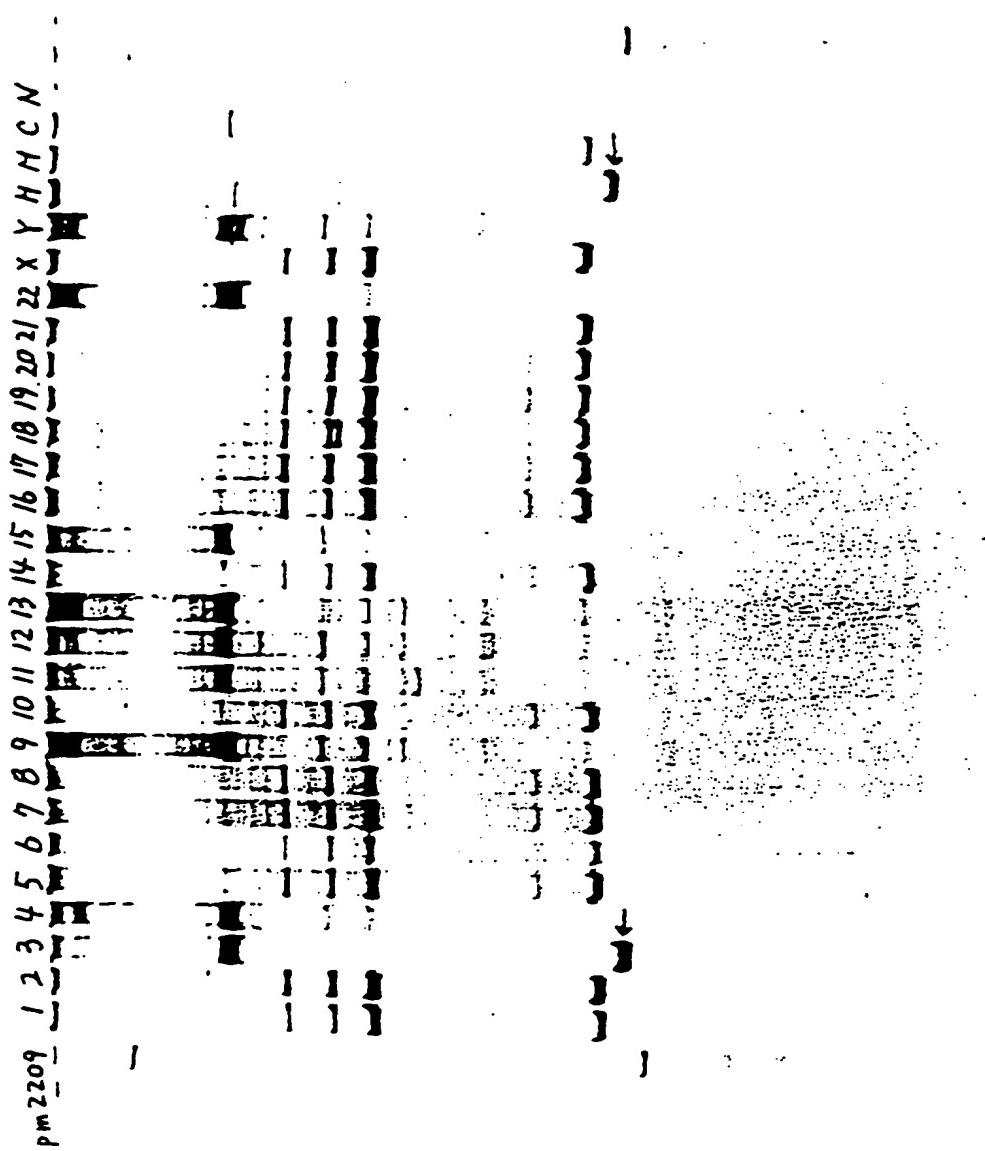


Fig. 12

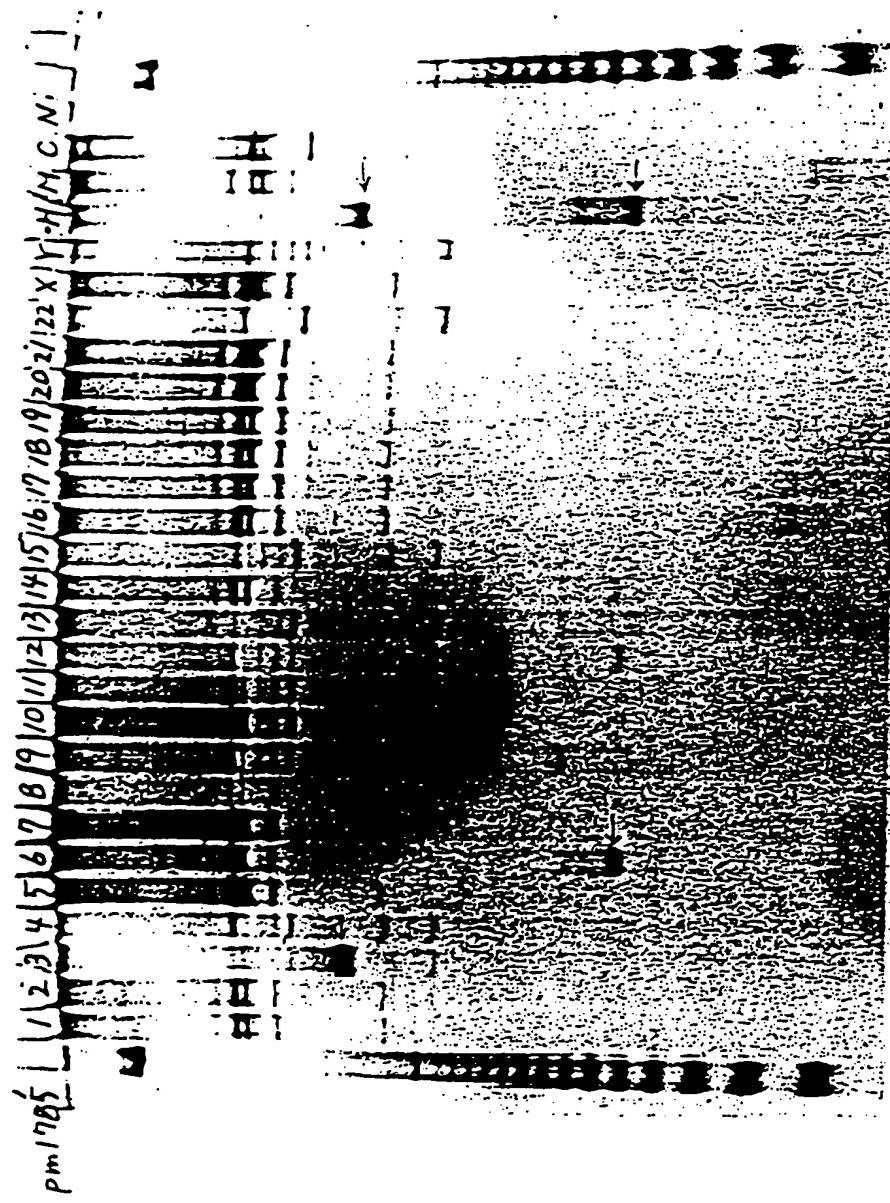


Fig. 13

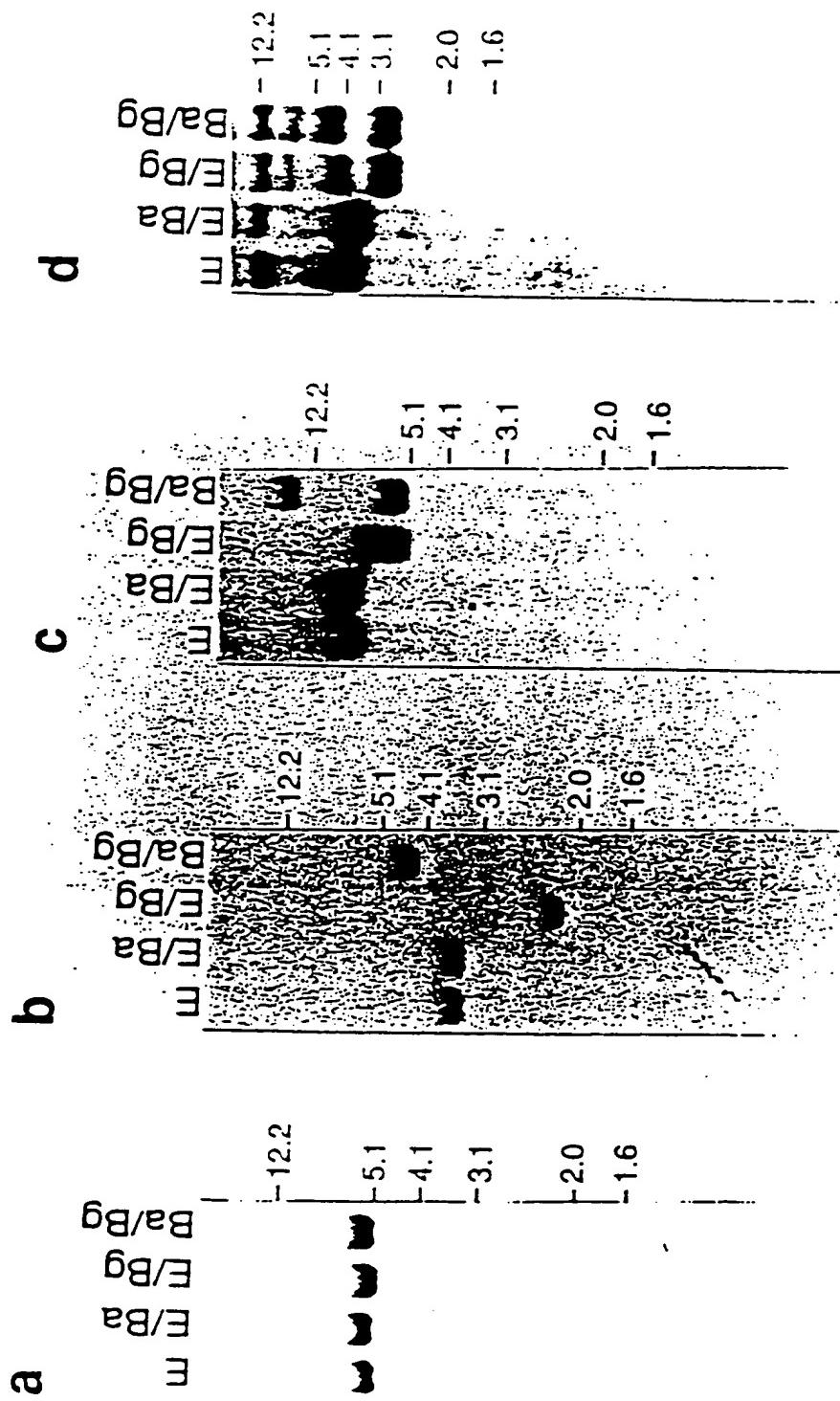


Fig. 14

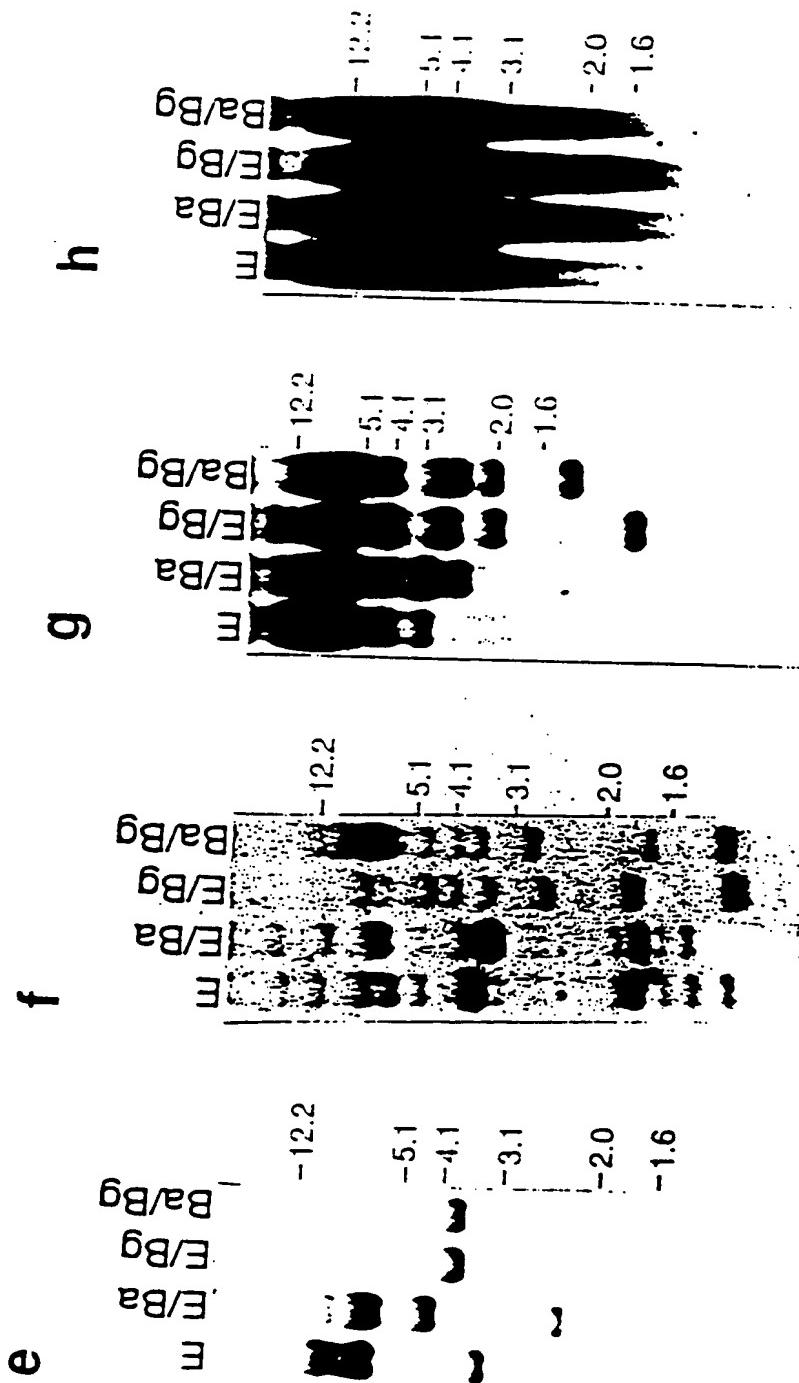


Fig. 15

## Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (3)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10496	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	61 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	61 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

a  
Chromosome

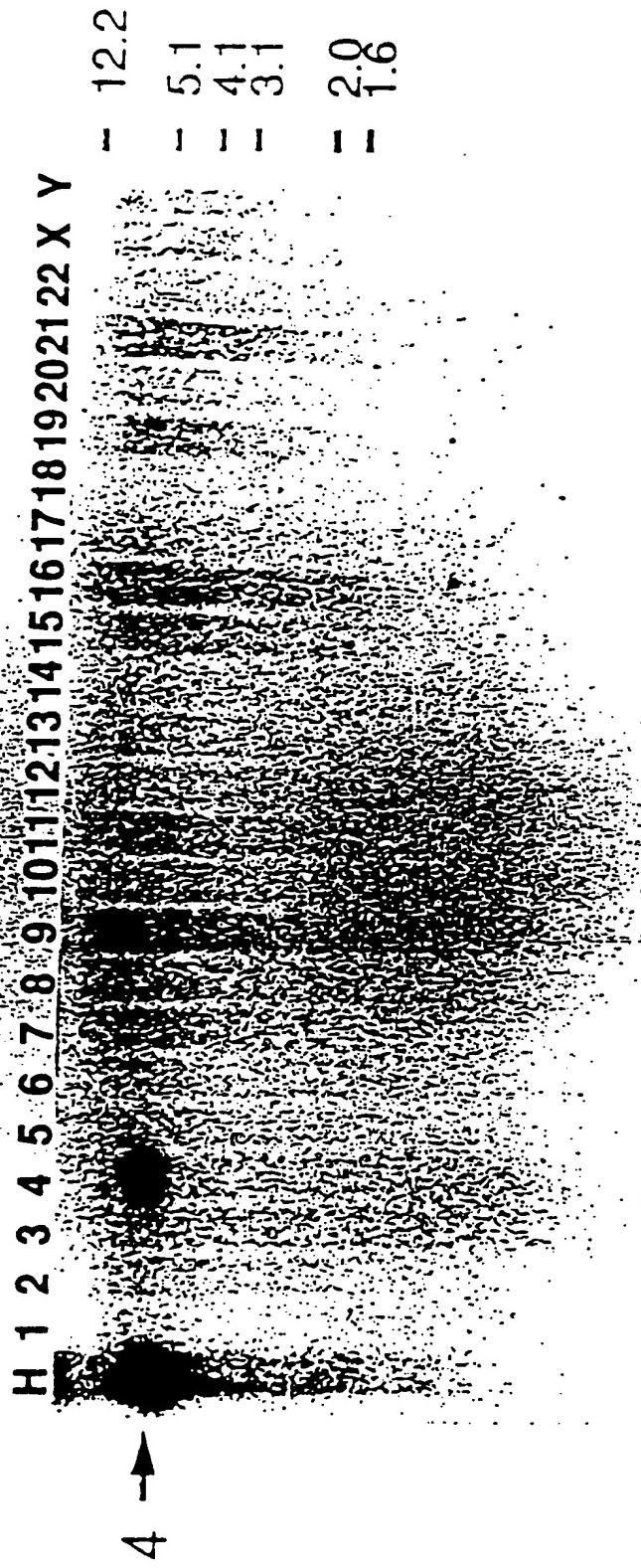


Fig. 17

b  
Chromosome

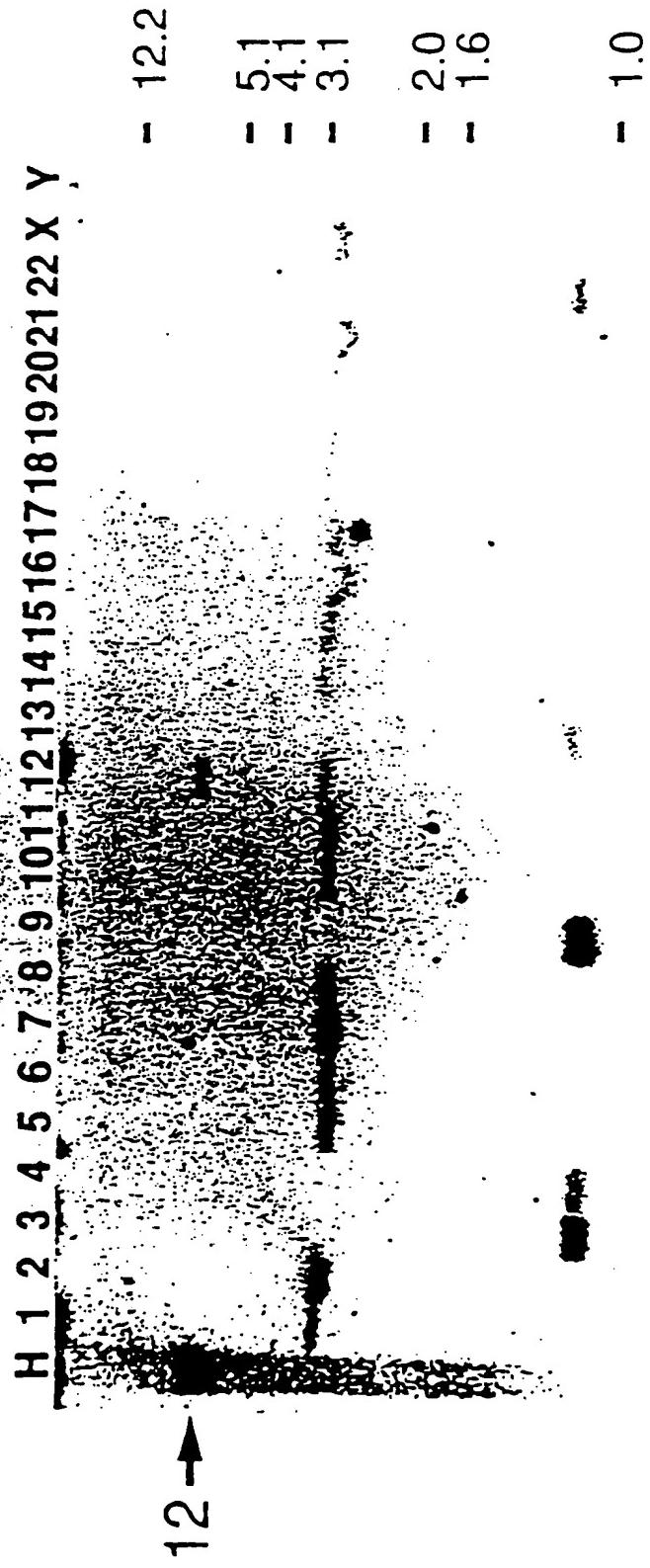


Fig. 18

C

Chromosome

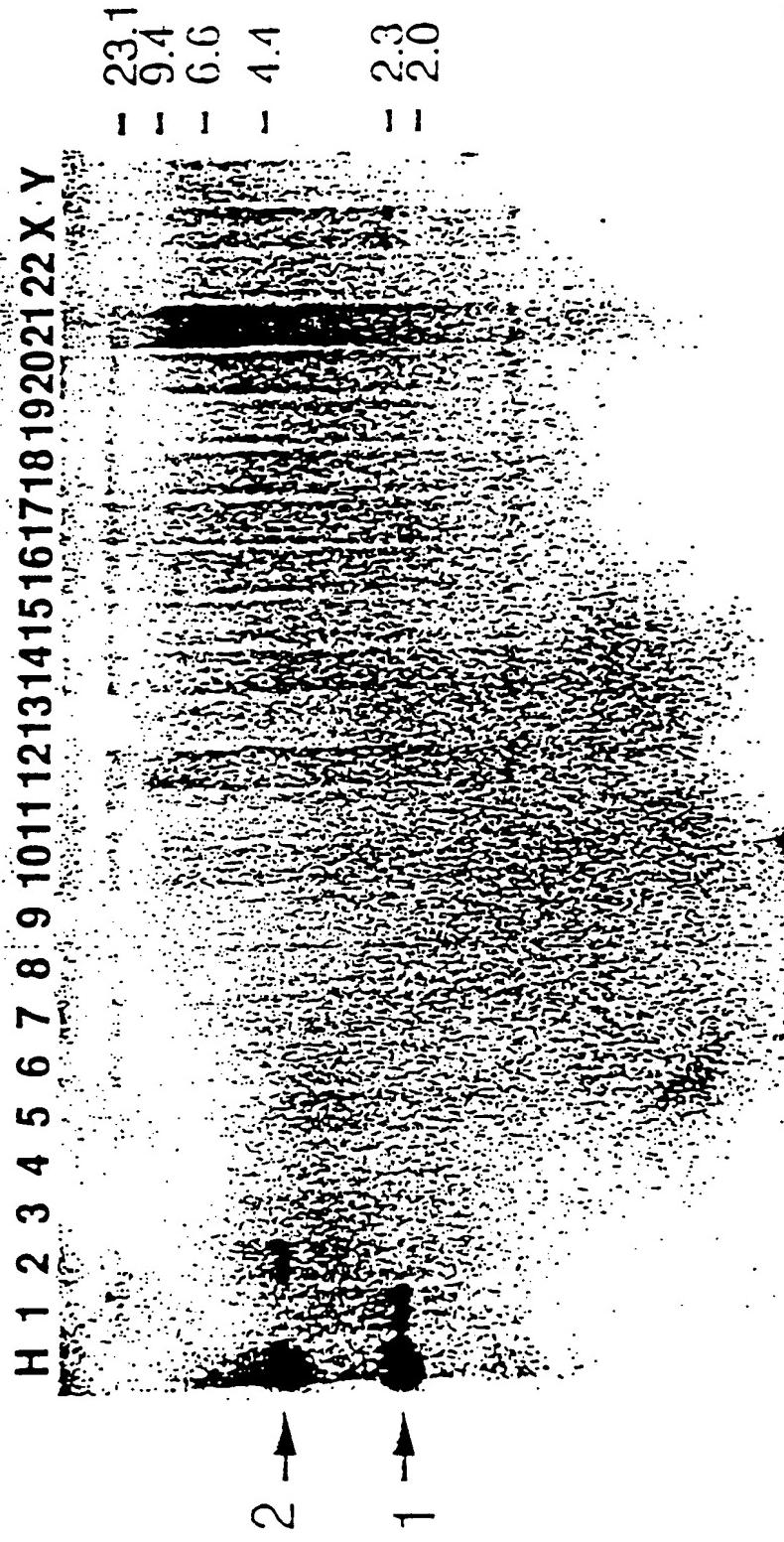
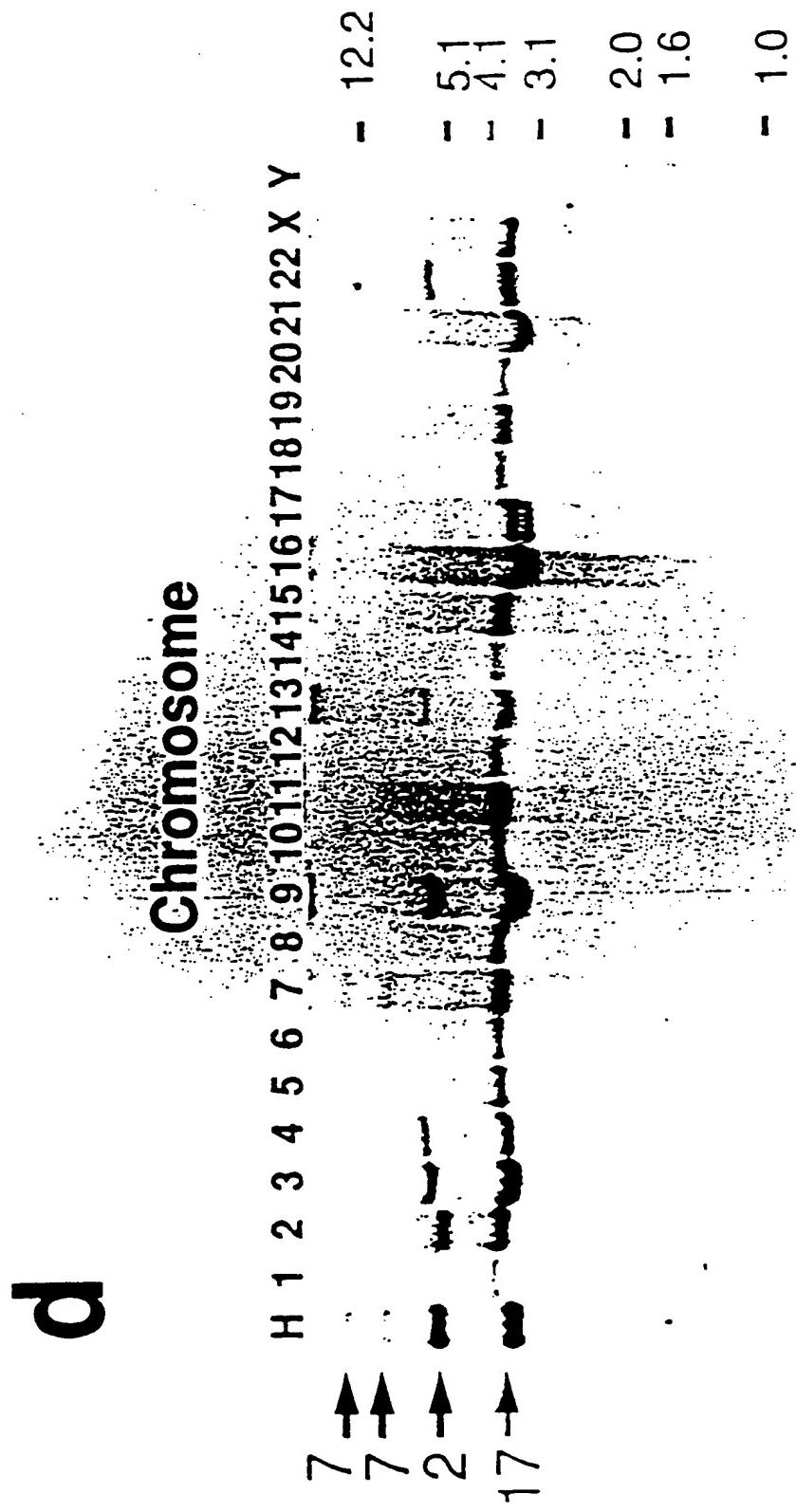


Fig. 19



e

# Chromosome

H 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

Fig. 20

EP 0 679 716 A1

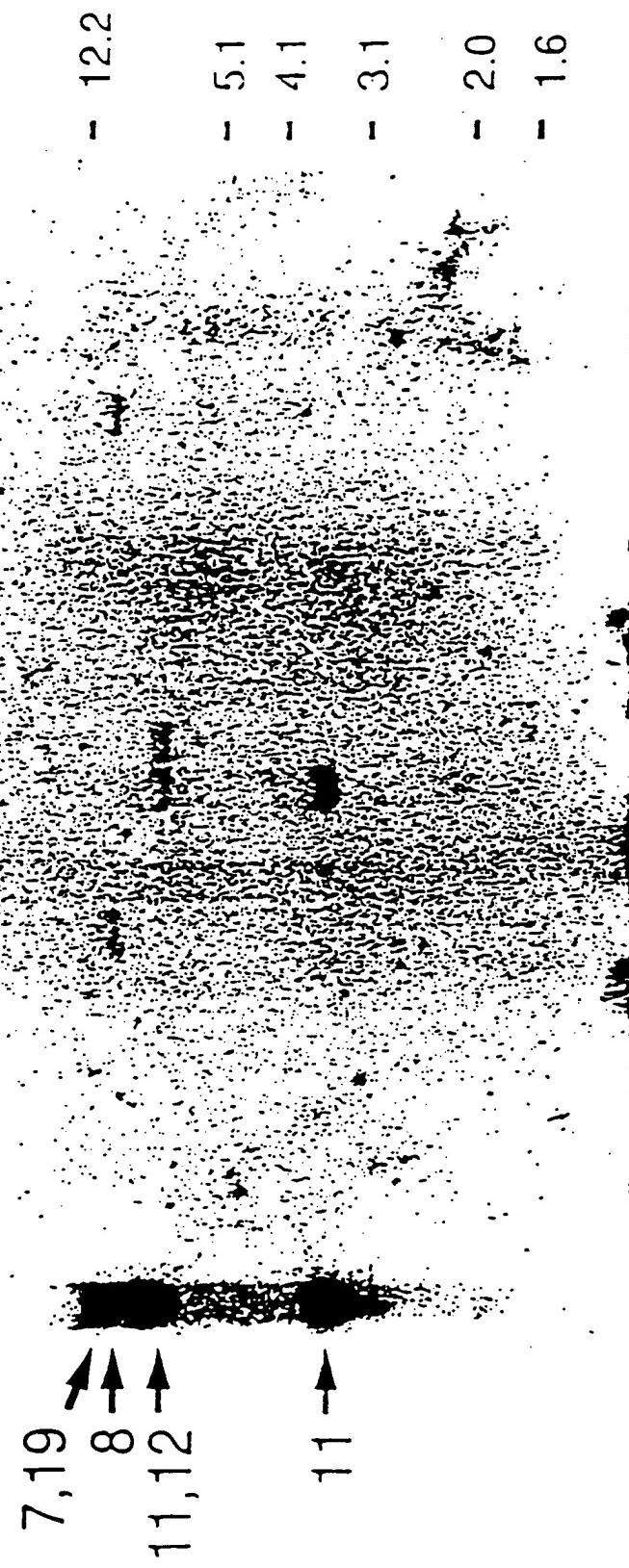


Fig. 21

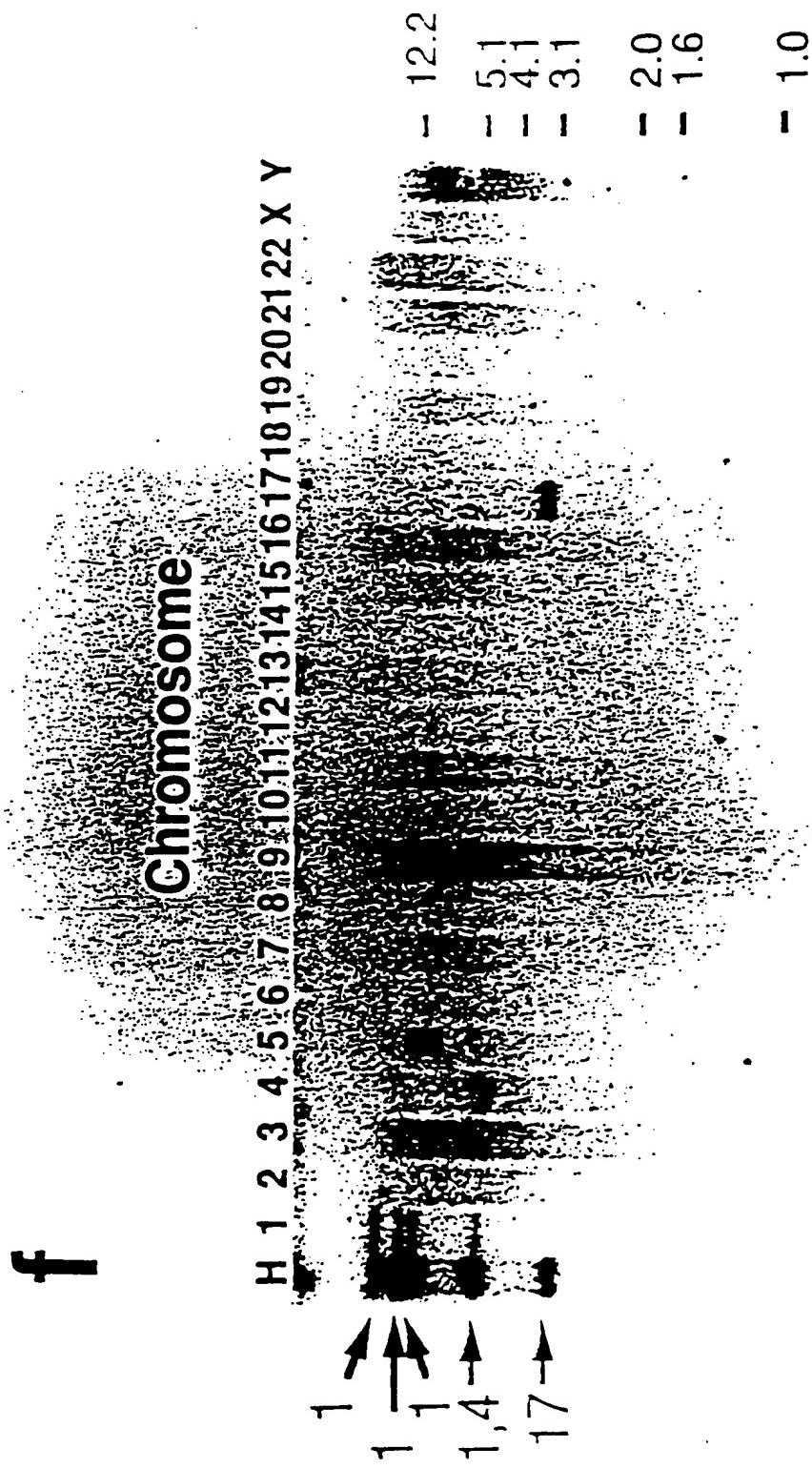


Fig. 22

g  
Chromosome

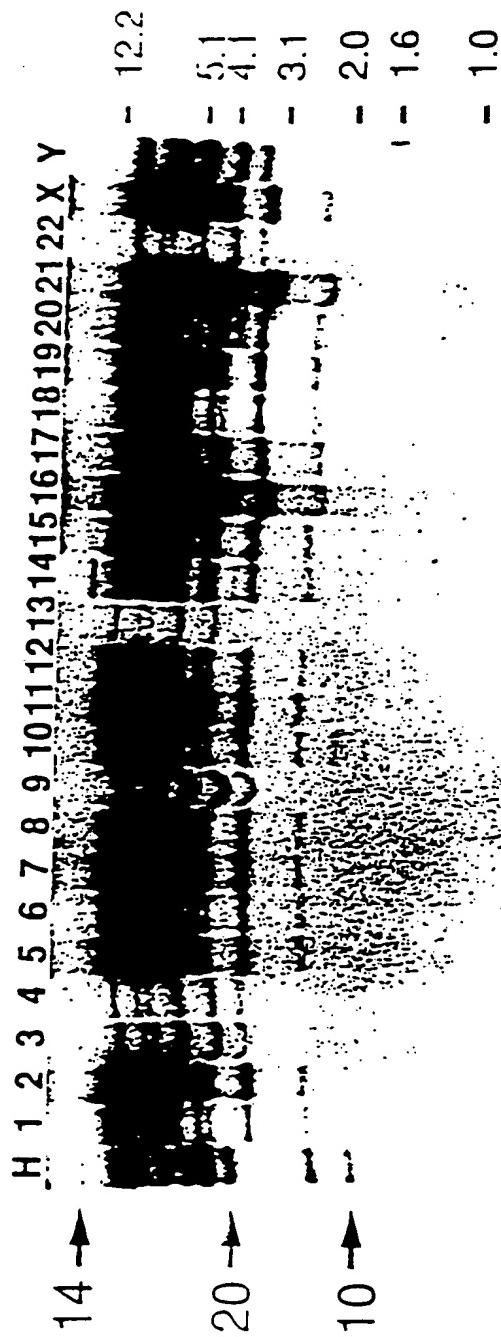


Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Clone	Sequence length	Numbers of bands detected with human whole chromosomes			Chromosomes assigned	Background	
		E/B	E/B <sub>1</sub>	E/B <sub>2</sub> ; B <sub>1</sub> /B <sub>2</sub>		Mouse	Chinese hamster
<b>Single band group:</b>							
c12e11	GS000075	432	1	1	1	9	0 0
c12e06	GS000062	540	1	1	1	6,15	0 0
c12g01	GS000280	212	1	1	1	2	1 1
c13c05	GS000117	359	1	1	1	11-	0 0
c13c07	GS000129	355	1	1	1	2	0 0
c13f10	GS000206	267	1	1	1	14	0 0
c13h01	GS000273	133	1	1	1	12-	0 0
c13h02	GS000222	167	1	1	1	6	0 0
d0gG2	GS000095	397	1	1	1	3	0 0
d0h07	GS000164	313	1	1	1	11	1 1
d1510	GS000348	153	1	1	1	20	0 0
hm01e12	GS000223	246	1	1	1	27	0 0
hm01e09	GS000423	157	0	1	1	1	0 0
hm01e12	junk	394	1	1	1	17	0 0
hm01e05	GS000068	454	1	1	1	19,22	0 0
hm01e10	GS000299	173	0	1	1	10	0 0
hm01g09	GS000053	477	1	1	1	6	0 0
hm01h07	GS000115	363	1	1	1	12	0 0
hm02a02	GS000130	344	1	1	1	4	0 0
hm02a04	GS000329	164	1	1	0	10	0 0
hm02e01	GS000293	271	1	1	1	15	0 0
hm02e01	GS000016	590	1	1	1	20	0 0
hm02e02	GS000342	156	0	1	1	14	0 0
hm02e05	GS000401	223	1	1	0	n.d.	0 0
hm02g02	GS000191	273	1	1	1	17	0 0
hm05e05	GS000251	219	1	1	1	6	2 0
hm05a10	junk	392	1	1	1	1	1 1
hm05c10	GS000009	606	1	1	1	1	0 0
km201	junk	169	1	1	1	n.d.	0 0
s10S	GS000001	703	1	1	1	5	0 0
s110	GS000057	471	1	1	1	3	0 0
s11d11	GS000307	#175	0	0	1	7	0 0
s11h01	GS000299	204	1	1	1	3	0 0
s147	GS000080	461	1	1	0	2	0 0
s14e06	junk	639	1	1	1	1	0 0
s14g02	GS000152	322	1	1	1	2	0 0
s14h12	GS000271	193	1	1	1	4	1 1
s150	GS000143	330	1	1	1	17	0 0
s15G	GS000002	306	1	1	1	2	1 1
s15b11	GS000250	221	1	1	1	14	0 0
s179	GS000273	196	1	1	1	n.d.	0 0
s246	GS000234	241	1	1	1	9	0 0
s247	GS000247	153	1	1	1	1	0 0
s270	junk	135	1	1	1	19	0 0

Fig. 24

Clone	Numbers of bands detected with human whole chromosomes						Chromosomes assigned	Background	
	Sequence length	ε	ε/3s <sub>1</sub>	ε/3s <sub>2</sub>	3s <sub>1</sub> /3s <sub>2</sub>	3s <sub>2</sub> /3s <sub>1</sub>		Chinese Mouse	Chinese hamster
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000265	207	1	1	0	1	6,15	1	1
s334	GS000165	112	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000295	130	1	1	1	1	n.d.	0	1
s443	GS000330	251	1	1	1	1	n.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s5L7	GS000334	161	1	1	1	1	14	1	1
s632	junk	537	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s550	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000218	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-43	GS000096	178	1	1	1	1	14	0	0
tw1-96	GS000138	339	1	1	1	1	11	0	0
Two band group :									
c12f12	GS000195	277	1	2	2	2	1,	1	1
c13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000181	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm05f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000083	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2,	1	2
s15e02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s254	GS000124	151	2	2	2	2	1,	3	1
s255	GS000235	219	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Clone		Sequence length	Numbers of bands detected with human whole chromosomes					Chromosomes assigned	Background	
			E	E/B <sub>1</sub>	E/B <sub>2</sub>	E/B <sub>3</sub>	B <sub>1</sub> /B <sub>2</sub>		Mouse	Chinese hamster
s311	GS000092	333	1	1	2	2		16.	1	1
s313	junk	132	2	2	1	0		20.	0	0
s317	GS000100	339	0	0	1	2		14,14	1	1
s336	GS000134	337	2	2	2	2		12,14	0	0
s333	GS000139	233	2	2	2	1		22,X	0	0
s339	GS000233	137	2	1	1	2		17.	0	0
s394	GS000063	449	2	1	2	2		13,14	0	0
s396	junk	277	2	2	2	2		17.	0	1
s455	junk	452	1	2	2	1		4.	0	0
s456	GS000236	132	2	2	2	2		8,10	1	2
s465	GS000201	274	1	1	2	2		6,15	0	0
s635	junk	250	1	1	1	2		9,13	0	0
s639	GS000257	205	1	2	2	2		2X	0	0
s656	GS000025	#590	2	2	0	2		6,11	0	0
tw1-33	junk	352	2	2	2	2		1.	0	0
tw1-39	GS000153	#321	2	2	2	2		17.	0	0
tw1-70	GS000061	441	1	1	2	1		11.	0	0
tw1-80	junk	453	2	2	1	2		9,17	2	2
tw1-87	GS000158	316	2	2	2	2		7.	0	0
<b>Three band group</b>										
d0h06	GS000030	417	3	3	3	1		1.	0	0
hm05b07	junk	336	2	3	3	3		5.	0	0
hm05g02	GS000209	267	2	2	2	1		3,17,19	1	1
s129	GS000107	378	3	3	3	3		n.d.	1	1
s173	GS000357	146	1	2	2	3		2.	0	0
s17a10	GS000294	131	3	3	3	3		2,13,22	1	1
s302	GS000412	638	2	2	2	3		X	1	1
s401	GS000224	249	2	1	3	3		6,5.	0	0
s654	GS000045	491	3	3	3	3		1,22.	0	0
tw1-82	GS000208	267	3	3	3	3		13.	4	0
<b>Four band group</b>										
c12g07	GS000154	320	4	4	2	3		5, 14,	0	0
c13a08	GS000055	508	3	3	4	4		2,7,7,17	1	2
c13c04	GS000106	#376	4	3	3	3		n.d.	0	2
c13e09	GS000302	195	4	2	4	4		2,17,	7	2
s136	GS000160	315	4	4	4	4		4X.	2	1
s163	GS000004	#618	4	4	4	2		4,4,8,20	3	1
s479	GS000130	293	4	4	2	2		7,8,11,11,12,19	0	0
<b>Group with 5 or more bands</b>										
c12f08	GS000253	217	5	5	5	2		2,7,9,14,	2	0
hc01	junk	374	12	12	15	13		1,2,6,	22	20
hd10	junk	361	4	4	4	8		n.d.	12	6
he10	junk	173	6	2	3	3		6,3,9,19,21,	3	3
hm01c05	GS000205	176	9	7	5	5		X	9	8
hm01f04	GS000246	215	8	10	5	5		n.d.	12	12
hm01g02	junk	411	9	6	6	4		10,14,20,	14	6

Fig. 26

Clone	Sequence length	Numbers of bands detected with human whole chromosomes					Chromosomes assigned	Background	
		E	E/B <sub>1</sub>	E/B <sub>2</sub>	E/B <sub>3</sub>	Mouse		Chinese hamster	
hm02f09	GS000273	442	9	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05z02	GS000096	373	5	6	4	6	2,3,17,	3	3
hm05z04	GS000236	#239	6	6	6	7	n.d.	3	5
kmb01	junk	350	3	5	5	5	13,	14	7
s1lf06	GS000319	170	6	6	6	4	1,2,2,3,4,6,13,15,	0	3
s14f01	GS000407	262	12	11	10	9	1,5,9,13,	6	3
s173	GS000094	397	5	4	6	3	1,1,1,1,4,17	0	0
s255	GS000323	167	10	12	11	14	13,	9	5
s341	junk	494	9	9	8	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,5,11,X,	3	5
tw1-63	junk	203	3	10	10	12	3,4,	17	11
<b>Bands no detected:</b>									
c13g02	GS000340	157	0	0	0	0	-	-	-
hm0le10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000105	360	0	0	0	0	-	-	-
s651	junk	510	0	0	0	0	-	-	-

## INTERNATIONAL SEARCH REPORT

International application No.

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## A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl<sup>6</sup> C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiations, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA: coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3- methylglutaryl coenzyme A reductase, and 3- hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)

 Further documents are listed in the continuation of Box C. See patent family annex.

## \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search  
February 6, 1995 (06. 02. 95)Date of mailing of the international search report  
March 7, 1995 (07. 03. 95)Name and mailing address of the ISA/  
Japanese Patent Office  
Facsimile No.

Authorized officer

Telephone No.

## INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
X	Gene, Vol. 93, 1990 Taanman, J. W., Schrage, C., Ponne, N., Das, A., Bolhuis, P. A., de Vries, H. and Agsteribbe, E. Isolation of cDNAs encoding Subunit VIb of human cytochrome c oxidase and steady-state levels of coxVIb mRNA in different tissues p. 285-291	1-6 (844)
X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
X	Immunogenetics, Vol. 32, 1990, Angelisova, P. et al. "The human leucocyte surface antigen CD53 is a protein structurally similar to the CD37 and MRC OX-44 antigens" p. 281-285	1-6 (1158)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Koken, M. H. et al. "Structural and functional conservation of two human homologs of the yeast DNA repair gene RAD6" p. 8865-8869	1-6 (1181)
X	Oncogene, Vol. 5, 1990, Firmbach-Kraft, I. et al. "Tyk 2, prototype of a novel class of non-receptor tyrosine Kinase genes" p. 1329-1336	1-6 (1345)
X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

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International application No.  
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X	J. Biol. Chem., Vol. 263, 1988, Luster, A. D. et al. "Molecular and biochemical characterization of a novel gamma-interferon-inducible protein" p. 12036-12043	1-6 (1455)
X	J. Clin. Invest., Vol. 83, 1989, Look, A. T. et al. "The human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N" p. 1299-1307	1-6 (1469)
X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
X	Nucleic Acids Res., Vol. 18, 1990, Liebhaber, S. A. et al. "Characterization of a human cDNA encoding a widely expressed and highly conserved cysteine-rich protein with an unusual zinc-finger motif" p. 3871-3879	1-6 (1642)
X	J. Biol. Chem., Vol. 264, 1989, Didsbury, J. et al. "Rac, a novel ras-related family of proteins that are botulinum toxin substrates" p. 16378-16382	1-6 (1709)
X	EMBO J., Vol. 6, 1987, Willison, K. et al. "The human homologue of the mouse t-complex gene, TCP1, is located on chromosome 6 but is not near the HLA region" p. 1967-1974	1-6 (1749)
X	J. Biol. Chem., Vol. 266, 1991, Wu, Y. et al. "Activation of globin gene expression by cDNAs from induced K562 cells: Evidence for involvement of ferritin in globin gene expression" p. 17566-17572	1-6 (1785)
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Fukumoto, H. et al "Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein" p. 5434-5438	1-6 (1878)

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X	J. Clin. Invest., Vol. 76, 1985, Cooke, N.E. et al. "Serum vitamin D-binding protein is a third member of the albumin and alpha fetoprotein gene family" p. 2420-2424	1-6 (1888)
X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxycytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
X	Gene, Vol. 44, 1986, Board, P. G. et al. "Molecular cloning and nucleotide sequence of human alpha-1 acid glycoprotein cDNA" p. 127-131	1-6 (1921)
X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)

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International application No.

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X	Biochemistry, Vol. 25, 1986, Koide, T. et al. "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA" p. 2220-2225	1-6 (2174)
X	Biochemistry, Vol. 22, 1983, Friezner-Degen, S. J. et al. "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin" p. 2087-2097	1-6 (2214)
X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
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X	Proc. Natl. Acad. Sci. U.S.A., Vol. 86, 1989, Sims, J. E. et al. "Cloning of the interleukin 1 receptor from human T cells" p. 8946-8950	1-6 (2265)
X	Eur. J. Biochem., Vol. 169, 1987, Mackinnon, C. M. et al. "Molecular cloning of cDNA for human complement component Cls. The complete amino acid sequence" p. 547-553	1-6 (2266)
X	J. Virol., Vol. 65, 1990, Tsujimoto, A. et al. "Isolation of cDNA for DNA binding proteins which specifically bind to TAX-responsive enhancer element in the LTR of HTLA-1" p. 1420-1426	1-6 (2475)
X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
X	Nature, Vol. 353, 1991, Kelly, A. P. et al. "A new human HLA class II-related locus, DM" p. 571-573	1-6 (2583)

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International application No.  
PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Hla, T. et al. "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors" p. 9308-9313	1-6 (2600)
X	J. Biol. Chem., Vol. 267, 1992, White, R. T. et al. "Human adipsin is identical to complement factor D and expressed at high levels in adipose tissue" p. 9210-9213	1-6 (2802)
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X	Nucleic Acids Res., Vol. 17, 1989, Sawada, R. et al. "Complementary DNA sequence and deduced peptide sequence for CD59/MEM43 antigen, the human homologue of murine lymphocyte antigen Ly-6c" p. 6728-6728	1-6 (2954)
X	DNA Cell Biol., Vol. 9, 1990, Sawada, R. et al. "Isolation and expression of the full-length cDNA encoding CD59 antigen of human lymphocytes" p. 213-220	1-6 (2954)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Weller, P. A. et al. "Complete sequence of human vinculin and assignment of the gene to chromosome 10" p. 5667-5671	1-6 (2983)
X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

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International application No.  
PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
X	Nucleic Acids Res., Vol. 20, 1992, Wintzerith, M. et al. "Sequence of the human RNA polymerase II largest subunit" p. 910-910	1-6 (3083)
X	J. Cell Biol., Vol. 103, 1986, Lawler, J. et al. "The Structure of Human Thrombospondin, an adhesive Glycoprotein with Multiple Calcium binding Sites and Homologies with Several Different Proteins" p. 1635-1648	1-6 (3266)
X	Nature, Vol. 352, 1991, Maslen, C. L. et al. "Partial sequence of a candidate gene for the marfan syndrome" p. 334-337	1-6 (3334)
X	J. Cell Biol., Vol. 111, 1990, Fishman, G. I. et al. "Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel" p. 589-598	1-6 (3403)
X	Cell, Vol. 40, 1985, Ebina, Y. et al. "The human insulin receptor cDNA: The structural basis for hormone-activated membrane signalling" p. 747-758	1-6 (3447)
X	Oncogene, Vol. 5, 1990, Westin, E. H. et al. "Alternative splicing of the human c-myb gene" p. 1117-1124	1-6 (3529)
X	Genomics, Vol. 4, 1989, Todd, S. et al. "cDNA sequence, interspecies comparison and gene mapping analysis of argininosuccinate lyase" p. 53-59	1-6 (3575)
X	FEBS Lett., Vol. 207, 1986, Codina, J. et al. "-Subunits of the human liver Gs/Gi signal-transducing proteins and those of bovine retinal rod cell transducin are identical" p. 187-192	1-6 (3796)
X	Nucleic Acids Res., Vol. 18, 1990, Roessler, B. J. et al. "Cloning of two distinct copies of human phosphoribosyl pyrophosphate synthetase cDNA" p. 193-193	1-6 (3828)

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International application No.

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## C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biochem., Vol. 109, 1991, Sonoda, T. et. al. "Complete nucleotide sequence of human phosphoribosyl pyrophosphate synthetase subunit I (PRS I) cDNA and a comparison with human and rat PRPS gene families" p. 361-364	1-6 (3828)
X	J. Biol. Chem., Vol. 263, 1988, Wermuth, B. et al. "Human carbonyl reductase: Nucleotide sequence analysis of a cDNA and amino acid sequence of the encoded protein" p. 16185-16188	1-6 (4033)
X	Biochim. Biophys. Acta. Vol. 1048, 1990, Forrest, G. L. et al. "Induction of a human carbonyl reductase gene located on chromosome 21" p. 149-155	1-6 (4033)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Schuetz, T. J. et al. "Isolation of a cDNA for HSF2: Evidence for two heat shock factor genes in humans' p. 6911-6915	1-6 (4093)
X	Nucleic Acids Res., Vol. 13, 1985, Hallewell, R. A. et al. "Human Cu/Zn superoxide dismutase cDNA: isolation of clones synthesising high levels of active or inactive enzyme from an expression library" p. 2017-2034	1-6 (4110)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 80, 1983, Sherman, L. et al. "Nucleotide sequence and expression of human chromosome 21 - encoded superoxide dismutase mRNA" p. 5465-5469	1-6 (4110)
X	J. Biol. Chem., Vol. 268, 1993, David, V. et al. "Interaction with newly synthesized and retained proteins in the endoplasmic reticulum suggests a chaperone function for human integral membrane protein IP90 (calnexin)" p. 9585-9592	1-6 (4373)
X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

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International application No.

PCT/JP94/01916

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Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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X	J. Biol. Chem., Vol. 263, 1988, Verma, A. K. et al. "Complete primary structure of a human plasma membrane Ca <sup>2+</sup> pump" p. 14152-14159	1-6 (4673)
X	J. Biol. Chem., Vol. 267, 1992, Shechter, I. et al. "Solubilization, purification and characterization of a truncated form of rat hepatic squalene synthetase" p. 8628-8635	1-6 (4818)
X	J. Biol. Chem., Vol. 267, 1992, Mckenzie, T. L. et al. "Molecular cloning, expression, and characterization of the cDNA for the rat hepataic squalene synthase" p. 21368-21374	1-6 (4818)
X	Nucleic Acids Res., Vol. 13, 1985, Furutani, Y. et al. "Cloning and characterization of the cDNAs for human and rabbit interleukin-1 precursor" p. 5869-5882	1-6 (4872)
X	Proc. Natl. Acad. Sci U.S.A., Vol. 89, 1992, Katoh, M. et al. "K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase" p. 2960-2964	1-6 (4914)
X	Differentiation, Vol. 42, 1989, Kuruc, N. et al. "Synthesis of cytokeratin 13, a component characteristic of internal stratified epithelia, is not induced in human epidermal tumors" p. 111-123	1-6 (5264)
X	J. Biol. Chem., Vol. 266, 1991, Kiefer, M. C. et al. "Identification and molecular cloning of two new 30-kDa insulin-like growth factor binding proteins isolated from adult human serum" p. 9043-9049	1-6 (5374)

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X	J. Biol. Chem., Vol. 265, 1990, Opiplari, A. W. et al. "The A20 cDNA induced by tumor necrosis factor alpha-encodes a novel type of zinc finger protein" p. 14705-14708	1-6 (5427)
X	J. Biol. Chem., Vol. 265, 1990, McLean, J. W. et al. "cDNA sequence of the human integrin beta-5 subunit" p. 17126-17131	1-6 (5715)
X	Cell, Vol. 66, 1991, Ge, H. et al. "primary structure of the human splicing factor ASF reveals similarities with drosophila regulators" p. 373-382	1-6 (5860)
X	Cancer Res., Vol. 52, 1992, Kondoh, N. et al. "Differential expression of S19 ribosomal protein, laminin binding protein and HLA class I mRNAs associated with colon carcinoma progression and differentiation" p. 791-796	1-6 (6439)
X	J. Biol. Chem., Vol. 263, 1988, Collart, F. R. et al. "Cloning and sequence analysis of the human and chinese hamster inosine-5'-monophosphate dehydrogenase cDNA" p. 15769-15772	1-6 (6471)
X	J. Biol. Chem., Vol. 261, 1986, Romeo, P. -H. et al. "Molecular cloning and nucleotide sequence of a complete human uroporphyrinogen decarboxylase cDNA" p. 9825-9831	1-6 (6569)
X	J. Cell Biol., Vol. 106, 1988, Leube, R. E. et al. "Molecular characterization and expression of the stratification-related cytokeratins 4 and 15" p. 1249-1261	1-6 (6875)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Daher, K. A. et al. "Isolation and characterization of human defensin cDNA clones" p. 7327-7331	1-6 (7106)
X	J. Exp. Med., Vol. 172, 1990, Larsen, A. et al. "Expression Cloning of a Human Granulocyte Colony-stimulating Factor Receptor: a Structural Mosaic of Hematopoietin Receptor, Immunoglobulin, and Fibronectin Domains" p. 1559-1570	1-6 (7126)

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International application No.

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A	Nature Genetics, Vol. 2, 1992, Okubo, K. et al. "Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression" p. 173-179	1-6
A	Nature Genetics, Vol. 2, 1992, Khan, A. S. et al. "Single pass sequencing and physical and genetic mapping of human brain cDNAs" p. 180-188	1-6

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